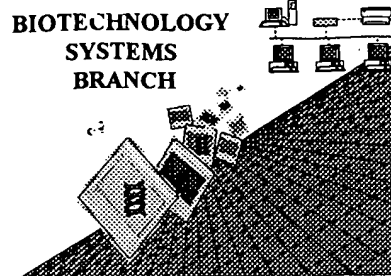


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/715,417
Source: OIPF
Date Processed by STIC: 7/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,417

DATE: 07/06/2001

TIME: 10:55:55

Input Set : A:\Cura1061.APP

Output Set: N:\CRF3\07062001\I715417.raw

3 <110> APPLICANT: Shimkets, Richard
 4 Lichenstein, Henri
 5 Vernet, Corine
 6 Fernandes, Elma
 8 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 10 <130> FILE REFERENCE: 15966-606
 12 <140> CURRENT APPLICATION NUMBER: 09/715,417
 13 <141> CURRENT FILING DATE: 2000-11-16
 15 <150> PRIOR APPLICATION NUMBER: 60/166,336
 16 <151> PRIOR FILING DATE: 1999-11-19
 18 <150> PRIOR APPLICATION NUMBER: 60/167,785
 19 <151> PRIOR FILING DATE: 1999-11-29
 21 <150> PRIOR APPLICATION NUMBER: 60/187,844
 22 <151> PRIOR FILING DATE: 2000-03-08
 24 <160> NUMBER OF SEQ ID NOS: 38
 26 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

1717 <210> SEQ ID NO: 29
 1718 <211> LENGTH: 3905
 1719 <212> TYPE: DNA
 1720 <213> ORGANISM: Homo sapiens
 1722 <400> SEQUENCE: 29

1723	ggatttgaga	gcctgaactt	agccatacac	cagatctacc	tttggaccgc	aaaagggacc	60
1724	cagtgttca	tgaagctggt	tttttttgtt	ttgttttgtt	ttttttccgt	tgttttgttt	120
1725	cggttttacc	aacctgactg	ggtgtttttc	aatatccacc	attcagactt	tcctcaacag	180
1726	cagaggatgt	ggcagtggca	aagacaaggg	gatgggggga	gacgaaaggg	aaaggggcct	240
1727	gcatgaaaga	ccatgtctgt	cttcctgctg	gtgccagttc	cctgaacctc	atcttgttgt	300
1728	tcagccctt	actgcagcct	gccagggcct	ccactccatg	gcttcacctc	aggccagacc	360
1729	agcaccagc	ccgggggctc	catccacttt	ggctgcaacg	ccggctaccg	cctgggtggga	420
1730	cacagcatgg	ccatctgtac	ccggcaccct	cagggtacc	acctgtggag	cgaagccatc	480
1731	cctctctgtc	aagctctttc	ctgtgggctt	cctgaggccc	ccaagaatgg	aatggtgttt	540
1732	ggcaaggagt	acacagtggg	aaccaaggcc	gtgtacagct	gcagtgaagg	ctaccacctc	600
1733	caggcaggcg	ctgaggccac	tgcagagtgt	ctggacacag	gcctatggag	caaccgcaat	660
1734	gtcccaccac	agtgtgtccc	tgtgacttgt	cctgatgtca	gtagcatcag	cgtggagcat	720
1735	ggccgatgga	ggcttatctt	tgagacacag	tatcagttcc	aggcccagct	gatgtctatc	780
1736	tgtgaccctg	gctactacta	tactggccaa	agggtcaccc	gctgtcaggc	caatggcaaa	840
1737	tggagcctcg	gggactctac	gcccacctgc	cgaatcatct	cctgtggaga	gctcccgtat	900
1738	ccccccaatg	gccaccgcat	cggaacactg	tctgtctacg	gggcaacagc	catcttctcc	960
1739	tgcaattccg	gatacacact	ggtgggctcc	aggggtgcgtg	agtgcattggc	caatgggctc	1020
1740	tggagtggct	ctgaagtccg	ctgccttgct	ggacactgtg	ggactcctga	gccattgtgc	1080
1741	aacggacaca	tcaatgggga	gaactacagc	taccggggca	gtgtggtgta	ccaatgcaat	1140
1742	gctggcttcc	gcctgatcgg	catgtctgtg	cgcatctgcc	agcaggatca	tcaatggctg	1200
1743	ggcaagacc	ctttctgtgt	gccaattacc	tgtggacacc	caggcaacc	tgtcaacggc	1260
1744	ctcactcagg	gtaaccagtt	taacctcaac	gatgtgggtca	agtttgtttg	caaccctggg	1320

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,417

DATE: 07/06/2001

TIME: 10:55:55

Input Set : A:\Cura1061.APP

Output Set: N:\CRF3\07062001\I715417.raw

```

1745 tatatggctg agggggctgc taggtcccaa tgccctggcca gcggggcaatg. gagtgcacatg 1380
1746 ctgcccacct gcagaatcat caactgtaca gacccctggac accaagaaaa tagtggttcgt 1440
1747 caggtccacg ccagcggccc gcacagggtc agcttcggca ccactgtgtc ttaccgggtgc 1500
E--> 1748 nnaaccacgg cttctacctc ctgggcaacc ccagtgtcca gctgccaggg agatggcaca 1560
1749 tgggaccgtc cccgccccca gtgtctcttg gtgtcctgtg gccatccggg ctccccgcct 1620
1750 cactcccaga tgtctggaga cagttatact gtgggagcag tgggtgcggtc cagctgcac 1680
1751 ggcaagcgta ctctgggtgg aaacagcacc cgcagtgtgt ggctggatgg acactggact 1740
1752 ggctccctcc ctcaactgtc aggaaccagc gtgggagttt gcggtgacct tgggatcccg 1800
1753 gctcatggca tccgtttggg ggacagcttt gatccaggca ctgtgatgcg cttcagctgt 1860
1754 gaagctggcc acgtgtcccg gggatcgta gagcgacct gtcaagccaa tggctcgtgg 1920
1755 agcggctcgc agcctgagtg tggagtgate tcttgtggga accctgggac tccaagtaat 1980
1756 gcccgagttg tgttcagtg tggcctgggt ttctccagct ctatcgtcta tgagtgcgg 2040
1757 gaaggatact acgccacagg cctgtcagc cgtcactgct cggtcacatg tacctggaca 2100
1758 ggcagtgacc ctgagtgcct cgtcataaac tgtggtgacc ctgggattcc agccaatggc 2160
1759 cttcggctgg gcaatgactt caggtacaa aaaactgtga catatcagtg tgtccctggc 2220
1760 tatatgatgg agtcacatag agtatctgt ctgagctgca ccaaggacct gacatggaat 2280
1761 ggaaccaagc ccgtctgcaa agctctcat tgcaagccac ctccgtcat ccccaatggg 2340
1762 aaggtggtgg ggtctgactt catgtggggc tcaagtgtga cttatgctg cctggagggg 2400
1763 taccagctct ccctgcccgc ggtgttcacc tgtgagggaa atgggtcctg gaccggagag 2460
1764 ctgcctcagt gtttccctgt gttctgogg gatccctgtg tcccgctccg tgggaggaga 2520
1765 gaggaccgag gcttctccta caggtcatct gtctccttct cctgccatcc ccctctggtg 2580
1766 ctggtgggct ctccacgcag gttttgccag tcagatggga catggagtgg caccagccc 2640
1767 agctgcatag atccgaccct gaccacgtgt gcggacctg gtgtgccaca gtttgggata 2700
1768 cagaacaatt ctcagggtc ccagggttga agcacagtcc tcttccgttg tcaaaaaggc 2760
1769 tacctgcttc agggctccac caccaggacc tgccctccaa acctgacctg gagtggaaac 2820
1770 ccacctgact gtgtccccc cactgcagg cagccagaga cgccaacgca tgccaacgct 2880
1771 ggggccctgg atttgccctc catgggttac acgtcatta ctctgccag gagggttct 2940
1772 ccctcaaggg tggctccgag caccgcacct gcaaggcgga tggcagctgg acaggcaagc 3000
1773 cgcccatctg cctggcagag gtccggccca gtgggagacc catcaacact gccggggagc 3060
1774 caccgctcac ccaagccttg attcctgggg atgtttttgc caagaattcc ctgtggaaa 3120
1775 gggcctatga ataccagggg aagaagcagc cagccatgct cagagtgact ggcttccaag 3180
1776 ttgccaacag caaggtcaat gccaccatga tcgaccacag tggcgtggag ctgcacttgg 3240
1777 ctggaactta caagaaagaa gattttcate tctactcca ggtgtaccag attacaggc 3300
1778 ctgtggagat ctttatgaat aagttcaaag atgatcact ggctttagat ggccatgtct 3360
1779 cgtcagagtc ctccggagcc accttcactt accaaggctc tgtcaagggc caaggcttgg 3420
1780 ggcagttcgg ctttcaaaga ctggacctca ggtgctgga gtcagacccc gagtccattg 3480
1781 gccgccactt tgcttccaac agcagctcag tggcagccgc gatccctgtg ctttctatcg 3540
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1783 ctttcaatgg ctatgtggc cagcagaaca ccaatgttcg ggccacattt gagaacccaa 3660
1784 tgtacgaccg caacatccag cccacagaca tcatggccag cgaggcggag ttcacagtca 3720
1785 gcacagtgtg cacagcagta tagccaccgc gctggccgc tttttttgct aggttgaact 3780
1786 ggtactccag cagccgcga agctggactg tactgtgcc atctcagctc actgcaacct 3840
1787 cctgcctga ttccctgcc tcagcctgcc gagtgcctgc gattgcaggc gcgcaccgcc 3900
E--> 1788 acnnt 3905

```

see item 9 on Ena Summary Sheet

PSI Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/715,417

DATE: 07/06/2001

TIME: 10:55:56

Input Set : A:\Cura1061.APP

Output Set: N:\CRF3\07062001\I715417.raw

L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1748 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:2240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:2369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:2405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:2441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/7/5417

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.